

GATGGGAACACGACGATCATTTGTCCACTATTTTGGCCCTGCTGGTGATTATCAACCTTGGAGTCTAT 70  
Asp Gly Asn Thr Thr Thr Ile Ile Val His Tyr Phe Cys Pro Ala Gly Asp Tyr Gln Pro Trp Ser Leu

GGATGTGGCCAAAAGACGGAGGTGGGGCTGAATACGATTTCATCAACCCGGCTGACTCTTTTGGAGCTGT 140  
Trp Met Trp Pro Lys Asp Gly Gly Ala Glu Tyr Asp Phe Asn Gln Pro Ala Asp Ser Phe Gly Ala Val

TGCAAGTGTGATATTCAGGAAACCCCAAGTCAGGTAGGAATTATCGTTCCGCACTCAAGATTGGACCCAAA 210  
Ala Ser Ala Asp Ile Pro Gly Asn Pro Ser Gln Val Gly Ile Ile Val Arg Thr Gln Asp Trp Thr Lys

GATGTGAGCGCTGACCGCTACATAGATTTAAGCAAAGGAAATGAGGTGIGGCTTGTAGAAGGAAACAGCC 280  
Asp Val Ser Ala Asp Arg Tyr Ile Asp Leu Ser Lys Gly Asn Glu Val Trp Leu Val Glu Gly Asn Ser

AAATTTTTTATAATGAAAAGATGCTGAGGATGCAGATGCAACCCGCTGTAAAGCAACGCCTTATTAGATGC 350  
Gln Ile Phe Tyr Asn Glu Lys Asp Ala Glu Asp Ala Ala Lys Pro Ala Val Ser Asn Ala Tyr Leu Asp Ala

TTCAAACCCAGGTGCTGGTTAAACTTAGCCAGCCGTTAACTCTTGGGGAAGNNNAAGCGGCTTTACGGTT 420  
Ser Asn Gln Val Leu Val Lys Leu Ser Gln Pro Leu Thr Leu Gly Glu Gly ?? Ser Gly Phe Thr Val

FIG. 1A

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CATGACGACAGCAATAAGGATATTCCAGTGACATCTGTGAAGGATGCAAGTCTTGGTCAAGATGTAA 490  
His Asp Asp Thr Ala Asn Lys Asp Ile Pro Val Thr Ser Val Lys Asp Ala Ser Leu Gly Gln Asp Val

CCGCTGTTTTGGCAGGTACCTTCCAACATAATTTTGGAGGTTCGGATTGGGCACCTGATAATCACAGTAC 560  
Thr Ala Val Leu Ala Gly Thr Phe Gln His Ile Phe Gly Gly Ser Asp Trp Ala Pro Asp Asn His Ser Thr

TTTATTAAAAAGGTGACTAACAACTCTCTAICAATCTCAGGAGATCTTCTCTGAAGGAAACTACCAATAT 630  
Leu Leu Lys Lys Val Thr Asn Asn Leu Tyr Gln Phe Ser Gly Asp Leu Pro Glu Gly Asn Tyr Gln Tyr

AAAGTGGCTTTAAATGATAGCTGGAATAATCCGAGTTACCCATCTGACAACATTAATTAAACAGTCCCIG 700  
Lys Val Ala Leu Asn Asp Ser Trp Asn Asn Pro Ser Tyr Pro Ser Asp Asn Ile Asn Leu Thr Val Pro

CCGGCGGTGCACACGTCACCTTTTTCGTATATTCCGTCACATCATGCAGTCTATGACACAATTAATAATCC 770  
Ala Gly Gly Ala His Val Thr Phe Ser Tyr Ile Pro Ser Thr His Ala Val Tyr Asp Thr Ile Asn Asn Pro

TAATGCGGATTTACAAGTAGAAAGCGGGGTAAACGGGATCTCGTGACGGTTACTCTAGGGGAAGATCCA 840  
Asn Ala Asp Leu Gln Val Glu Ser Gly Val Lys Thr Asp Leu Val Thr Val Thr Leu Gly Glu Asp Pro

FIG. 1B

910  
GATGTGAGCCATACTCTGTCCATTCAAAACAGATGGCTATCAGGCAAGCAGGTGATACCTCGTAATGTGC  
Asp Val Ser His Thr Leu Ser Ile Gln Thr Asp Gly Tyr Gln Ala Lys Gln Val Ile Pro Arg Asn Val

980  
TTAATTCACAGTACTACTATTTCAGGAGATGATCTTGGGAATACCTATACACAGAAAGCAACAACCTT  
309 Y  
Leu Asn Ser Ser Gln Tyr Tyr Tyr Ser Gly Asp Asp Leu Gly Asn Thr Tyr Thr Gln Lys Ala Thr Thr Phe

1050  
TAAAGTCTGGGCACCAACTTCTACTCAAGTAAATGTTCTTCTTTATGACAGTGCAACGGGTTCTGTAAACA  
VWAP  
Lys Val Trp Ala Pro Thr Ser Thr Gln Val Asn Val Leu Leu Tyr Asp Ser Ala Thr Gly Ser Val Thr

1120  
AAAATCGTACCTATGACGGCATCGGGCCATGGTGTGGGAAGCAACGGTTAATCAAAACCTTGAAAAATT  
Lys Ile Val Pro Met Thr Ala Ser Gly His Gly Val Trp Glu Ala Thr Val Asn Gln Asn Leu Glu Asn

1190  
GGTATTACATGTATGAGGTAAACAGGCCAAGGCTCTACCCGAACGGCTGTGTGATCCTTATGCAACTGCGAT  
391 DPY  
Trp Tyr Tyr Met Tyr Glu Val Thr Gly Gln Gly Ser Thr Arg Thr Ala Val Asp Pro Tyr Ala Thr Ala Ile

1260  
TGCACCAAAATGGAACGAGAGGCATGATTGTGGACCTGGCTAAACACAGATCCTGCTGGCTGGAACAGTGAT  
Ala Pro Asn Gly Thr Arg Gly Met Ile Val Asp Leu Ala Lys Thr Asp Pro Ala Gly Trp Asn Ser Asp

FIG.-1C

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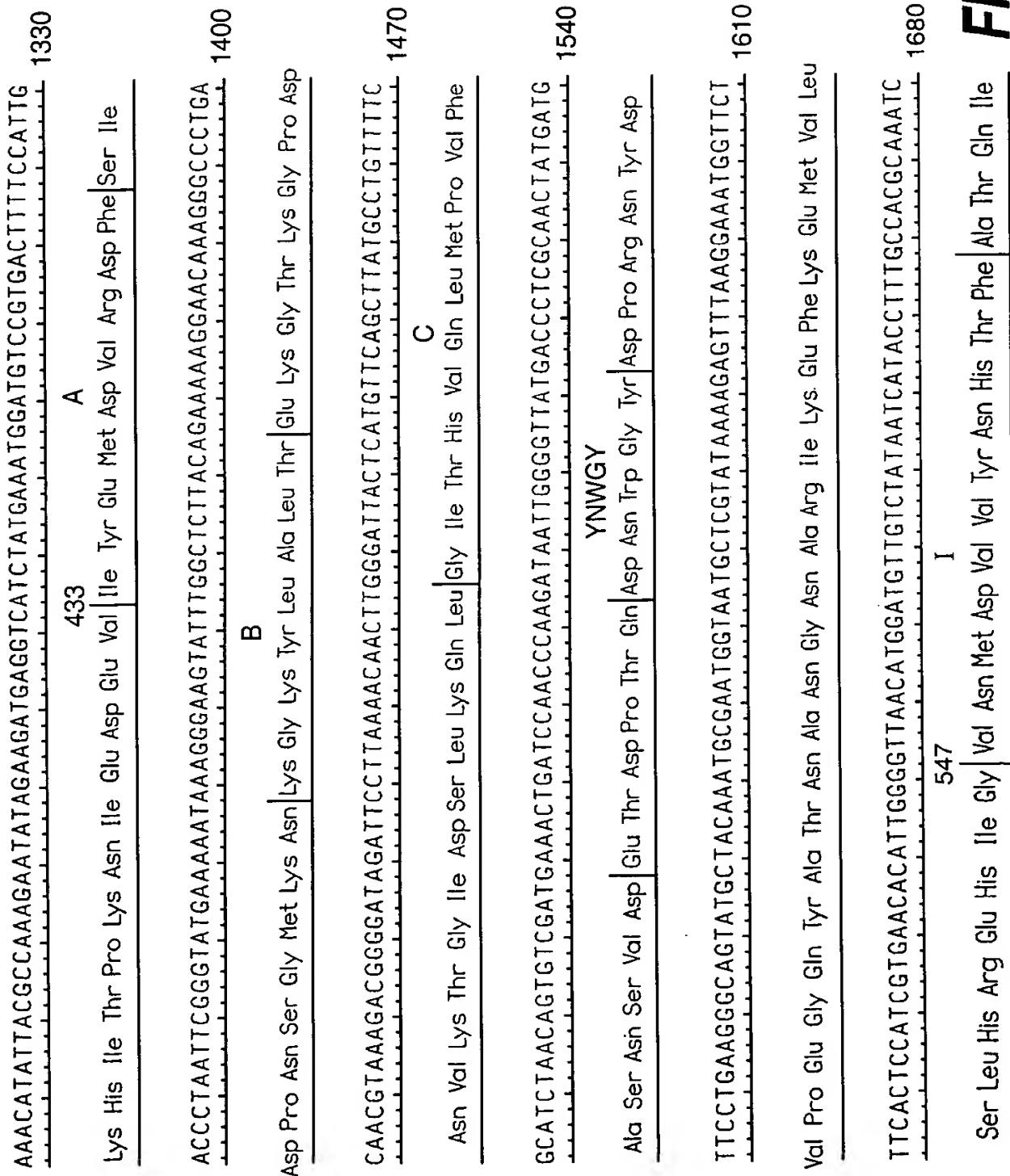


FIG. 1D

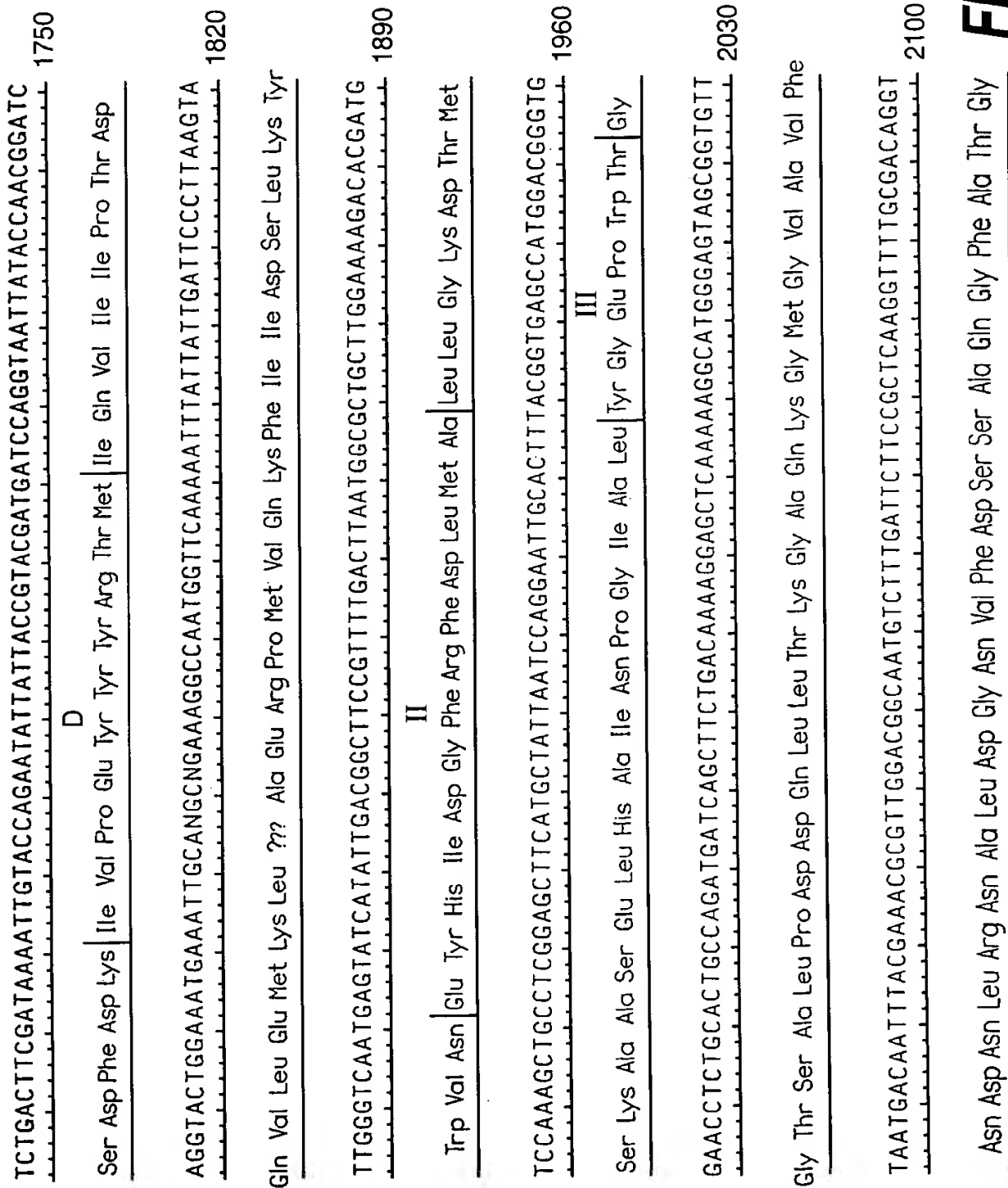


FIG. 1E

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2170  
GCAACAGGCTTAACTGATGCAATTAAGAAATGGCGTTGAGGGGAGTATTAAATGACTTTIACCTCTTCACCAG  
Ala Thr Gly Leu Thr Asp Ala Ile Lys Asn Gly Val Glu Gly Ser Ile Asn Asp Phe Thr Ser Ser Pro

2240  
GTGAGACAAATAACTATGTCACAAGTCATGATACTACACCCCTTIGGGACAAAATAGCCCTAAGCAATCC  
IV  
Gly Glu Thr Ile Asn Tyr Val Thr Ser His Asp Asn Tyr Thr Leu Trp Asp Lys Ile Ala Leu Ser Asn Pro

2310  
TAATGATTCCGAAGCGGATCGGATTAAAATGGATGAACTCGCACAAAGCAGTTGTTATGACCTCACAAGGC  
E  
Asn Asp Ser Glu Ala Asp Arg Ile Lys Met Asp Glu Leu Ala Gln Ala Val Val Met Thr Ser Gln Gly

2380  
GTTCCATTCAATGCAAGCGGGGAAGAAATGCTTCGTANAAAAGCGGCAACGACAATAGTTATAATGCAG  
Val Pro Phe Met Gln Gly Glu Glu Met Leu Arg ?? Lys Gly Gly Asn Asp Asn Ser Tyr Asn Ala

2450  
GCGATGCGGTCAATGAGTTTGATTGGAGCAGGAAAGCTCAATATCCAGATGTTTTCAACTATTATAGCGG  
Gly Asp Ala Val Asn Glu Phe Asp Trp Ser Arg Lys Ala Gln Tyr Pro Asp Val Phe Asn Tyr Tyr Ser Gly

2520  
GCTAATCCACCTTCGTCTTGATCACCACCGCCTTCGCGCATGACGACAGCTAATGAAAATCAATAGCCACCCTC  
Leu Ile His Leu Arg Leu Asp His Pro Ala Phe Arg Met Thr Thr Ala Asn Glu Ile Asn Ser His Leu

FIG. 1F

CAATTCCTAAATAGTCCAGAGAACACAGTGGCCTAIGAACTTAAGTCAATGTTAATAAGACAAATGGG 2590  
Gln Phe Leu Asn Ser Pro Glu Asn Thr Val Ala Tyr Glu Leu Thr Asp His Val Asn Lys Asp Lys Trp

GAAATATCATTTGTTTATAACCCCAATAAAACTGTAGCAACCATCAATTTGCCGAGCGGGGAAATGGGC 2660  
Gly Asn Ile Ile Val Val Tyr Asn Pro Asn Lys Thr Val Ala Thr Ile Asn Leu Pro Ser Gly Lys Trp Ala

AATCAATGCTACGAGCGGTAAAGTAGGAGAAATCCACCCTTGGTCAAGCAGAGGGGAAGTGTCCTCAAGTACCA 2730  
Ile Asn Ala Thr Ser Gly Lys Val Glu Ser Thr Leu Gly Gln Ala Glu Gly Ser Val Gln Val Pro

GGTATATCTATGATCCTTCATCAAGAGGTAAGCCACGACCACCGGTAAAAAGTAATAGAAAA 2794  
Gly Ile Ser Met Met Ile Leu His Gln Glu Val Ser Pro Asp His Gly Lys Lys

**FIG. 1G**

	10	20	30	40	Majority
M X X X X X X X X X L V L X X X F X X X G X S X X X X X T - - - Y					
A K K L I Y V C L S V C L V L T W A F N V K G Q S A H A D G N T T T I V H Y					
M L R Y T R N A L V L G S L V L L S G C D - N G S S S S S G N P D T - - - -					
M - - - - - - - - - V S I R R S F E A - - - - - - - - - Y					
- - - - X D X Q X X X X X X - P X X X X X X E X X - - X X X X X X V X X X D					
F C P A G D Y Q P W S L W M W P K D G G A E Y D F N Q P A D S F G A V A S A D					
- - - - P D N Q D V V R L - P D V A V P G E A V - - T A V E N Q A V I H L V D					
- V D D M N					
I X G X X S X X X X X X X X - - - W X K E X X X X X X X X X X V X X					
I P G N P S Q V G I I V R T Q D - - - W T K D V S A D R Y I D L S K G N E V W L					
I A G I T S S S A A D Y S S K N L Y L W N N E T C D A L S A P V A D W N D V S T					
I - - - - - I T V L I P A E Q - - - - - K E I - - - - - - - - - -					
X X X X S X P					
V E G N S Q I F Y N E K D A E D A A K P A V S N A Y L D A S N Q V L V K L S Q P					
T P S G S D K Y G P Y W V I P L N K E S G C I N V I V R D G T D K L I D S - - -					
- M T P P					

**FIG.-2A**



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	X X L X X X X D F T	- - - - -	X X X X P V X X X X X S L X X X X X X X X	Majority
	170	180	190	200
158	L T L G E G X S G F T V H D D T A N K D I P V T S V K D A S L G Q D V T A V L A			pullseqsig.seq.PRO
145	- D L R V A F G D F T - - - - -	- D R T V S V - I A G N S A V Y D S R A D A F R		klebpnseqsig.seq. pro
34	F R L E T E I T D F - - - - -	- P L A V R E E Y S L - - - - -		subpull.seq.pro
	X X F X X X X X X X W X - - - - -	X X X T L L - - - - -	X K X X X X L Y - - - - -	Majority
	210	220	230	240
198	G T F Q H I F G G S D W A P D N H S T L L - - - - -	- K K V T N N L Y Q F S G D L		pullseqsig.seq.PRO
177	A A F G V A L A E A H W V - - - - -	D K N T L L W P G G Q D K P I V R L Y - - - - -		klebpnseqsig.seq. pro
54	- - - - -	- - - - -	- - - - -	subpull.seq.pro
	- E X X Y X Y X X X X X X - - - - -	X X X X X X X X L T V X X X X X X V T F X X		Majority
	250	260	270	280
233	P E G N Y Q Y K V A L N D S W N N P S Y P S D N I N L T V P A G G A H V T F S Y			pullseqsig.seq.PRO
209	- - - - -	Y S H S S K V A A D - G E G K F T D R Y L K L T P T V S Q V S M R F		klebpnseqsig.seq. pro
54	- E A K Y K Y - - - - -	- - - - -	- - - - -	subpull.seq.pro
	I H X X X A X Y X X X X X P X - - - - -	X X X V X S G X K T D L V X X A X X E D X X X X		Majority
	290	300	310	320
273	I P S T H A V Y D T I N N P N A D L Q V E S G V K T D L V T V T L G E D P D V S			pullseqsig.seq.PRO
244	P H - - - - -	L S S Y A A F K L P D - N A N V D E L L Q G E T V A I A A A E D G I L I		klebpnseqsig.seq. pro
72	I H C V R A - - - - -	- - - - -	- S S G H K T D L Q I G A V - - - - -	subpull.seq.pro

FIG.\_2B

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	X X X X I Q T A G X X X	330	- - - - - V L X X X X Y Y X G E X L - - G A X Y T	340	Y	350	Majority
313	H T L S I Q T D G Y Q A K Q V I P R N V L N S S Q Y	330	Y Y S G D D L - - G N T Y T	340	Y	350	pullseqsig.seq.PRO
281	S A T Q V Q T A G - - - - - V L D D A - Y A E A A E A L S Y G A Q L A	330	Y Y S G D D L - - G N T Y T	340	Y	350	klebpnseqsig.seq.pro
91	- - - I R T A A F D D - - - - - - - - - E F Y Y D G E - L - - G A V Y T	330	Y Y S G D D L - - G N T Y T	340	Y	350	subpull.seq.pro
	X X X T T F K V W A P T A T Q V X X V X L Y X X X X X X X M T X S X X G	330	Y Y S G D D L - - G N T Y T	340	Y	350	Majority
	V W A P	370	380	390	400		
351	Q K A T T F K V W A P T S T Q V N V L L Y D S A T G S V T K I V P M T A S G H G	370	380	390	400		pullseqsig.seq.PRO
310	D G G V T F R V W A P T A Q Q V D V V Y S A D K K V I G S H P M T R D S A S G	370	380	390	400		klebpnseqsig.seq.pro
112	A D H T V F K V W A P A A T S A A V K L S H P N K S G - - R T F Q M T R L E K G	370	380	390	400		subpull.seq.pro
	V W X X T V X X D L X G X X Y X X X T X - X X X X R - - - E X V D P Y A X	370	380	390	400		Majority
		410	420	430	440		
391	V W E A T V N Q N L E N W Y Y M Y E V T G - Q G S T R - - - T A V D P Y A T	410	420	430	440		pullseqsig.seq.PRO
350	A W S W Q G G S D L K G A F Y R Y A M T V Y H P Q S R K V E Q Y E V T D P Y A H	410	420	430	440		klebpnseqsig.seq.pro
150	V Y A V T V T G D L H G Y E Y L F C I C N - N S E W M - - - E T V D Q Y A K	410	420	430	440		subpull.seq.pro
	A X X X N G E X G X V V D L X X X D - - P X G W X X X X P X X X X X D X V -	410	420	430	440		Majority
		450	460	470	480		
425	A I A P N G T R G M I V D L A K T D - - P A G W N S D K H I T P K N I E D E V -	450	460	470	480		pullseqsig.seq.PRO
390	S L S T N S E Y S Q V V D L N D S A L K P D G W D N L T M P H A Q K T K A D L A	450	460	470	480		klebpnseqsig.seq.pro
184	A V T V N G E K G V V L - - - R P D - - Q M K W T A P L K P F S H P V - D A V -	450	460	470	480		subpull.seq.pro

FIG.\_2C

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Majority									
- - - I Y E X H X R D F S I - D X N S G M X N K G K Y L A L T E X D T X X X X X									
A 490 500 510 520									
pullseqsig.seq.PRO									
klebpnseqsig.seq. pro									
subpull.seq.pro									
Majority									
X K T G X X L K X L G V T H V E L L P V F D X A X V D E - - - - -									
C 530 540 550 560									
pullseqsig.seq.PRO									
klebpnseqsig.seq. pro									
subpull.seq.pro									
Majority									
- - - - - 570 580 590 600									
pullseqsig.seq.PRO									
klebpnseqsig.seq. pro									
subpull.seq.pro									
Majority									
X P - - - - - T D X Y N W G Y D P X H Y X V P E G S Y A T N P X G X									
610 620 630 640									
pullseqsig.seq.PRO									
klebpnseqsig.seq. pro									
subpull.seq.pro									
YNWGY									

FIG.\_2D

**FIG.-2E**

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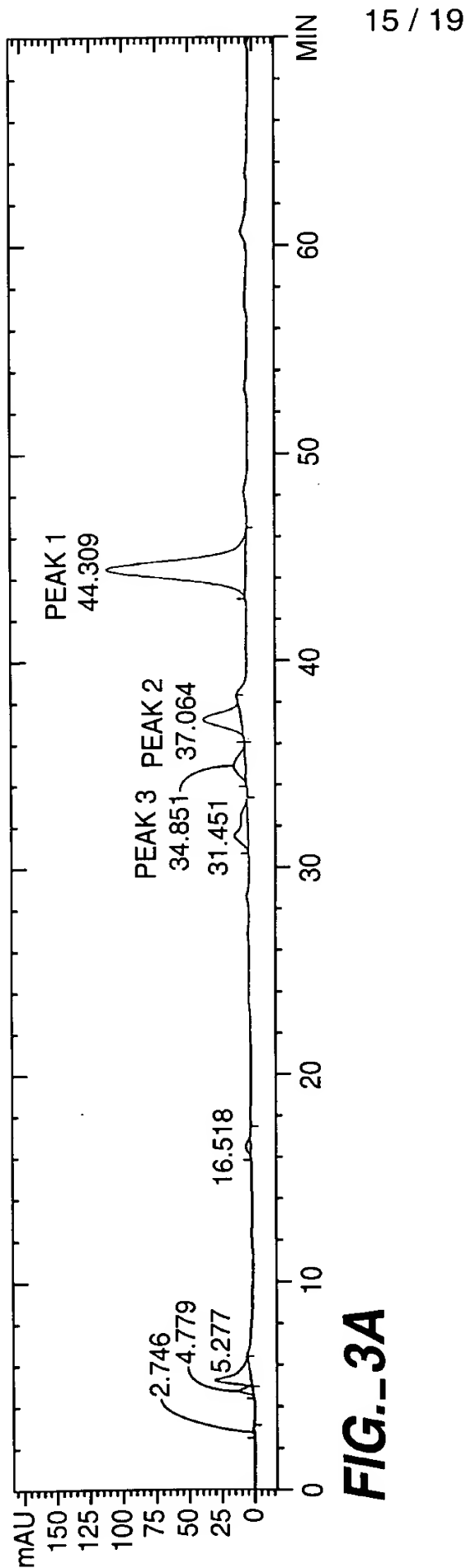
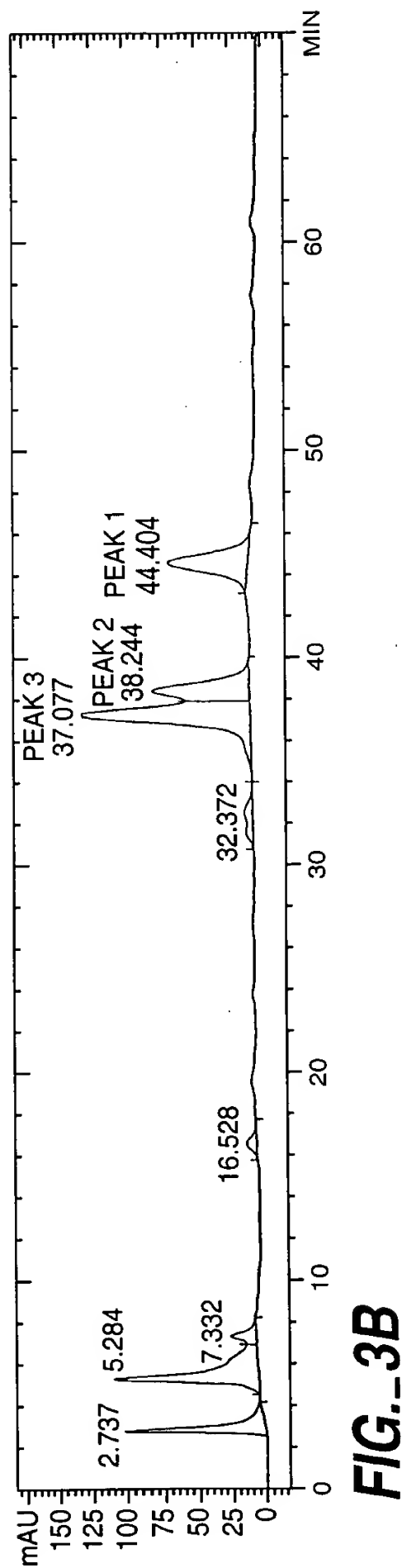
	L R D A V X G N X - F D S X A - - - - Q G F A X G A G X L X X A X - - - - -	Majority
	810 820 830 840	
710	L R N A L D G N V - F D S S A - - - - Q G F A T G A T G L T D A I - - - - -	pullseqsig.seq.PRO
743	L R D S V R G G P F D S G D A L R Q N Q G I G S G A G V L P N E L A S L S D D	klebpnseqsig.seq. pro
467	F R D A V K G N T - F H L K A - - - - T G F A L G N G E S A Q A V - - - - -	subpull.seq.pro
	- - - - - X X G X A G S - - - - - X X X K - - - - - A	Majority
	850 860 870 880	
738	- - - - - K N G V E G S -	pullseqsig.seq.PRO
783	Q V R H L A D L T R L G M A G N L A D F V M I D K D G A A K K G S E I D Y N G A	klebpnseqsig.seq. pro
495	- - - - - M H G I A G S - - - - - - - - - - S G W K - - - - - A	subpull.seq.pro
	X X X X X X P X E X I N Y V X S H D N X T L W D K I S X X X P Q E X D - A X R	Majority
	890 900 910 920	
745	I N D F T S S P G E T I N Y V T S H D N Y T L W D K I A L S N P N D S E - A D R	pullseqsig.seq.PRO
823	P G G Y A A D P T E V V N Y V S K H D N Q T L W D M I S Y K A S Q E A D L A T R	klebpnseqsig.seq. pro
507	L A P I V P E P S Q S I N Y V E S H D N H T F W D K M S F A L P Q E N D - S R K	subpull.seq.pro
	X X M Q X L A X A X V M L X Q G V P F X Q X G X E X L R X K X G X X N S Y X S G	Majority
	930 940 950 960	
784	I K M D E L A Q A V V M T S Q G V P F M Q G G E E M L R X K G N D N S Y N A G	pullseqsig.seq.PRO
863	V R M Q A V S L A T V M L G Q G I A F D Q Q G S E L L R S K S F T R D S Y D S G	klebpnseqsig.seq. pro
546	R S R Q R L A V A I I L L A Q G V P F I H S G Q E F F R T K Q G V E N S Y Q S S	subpull.seq.pro

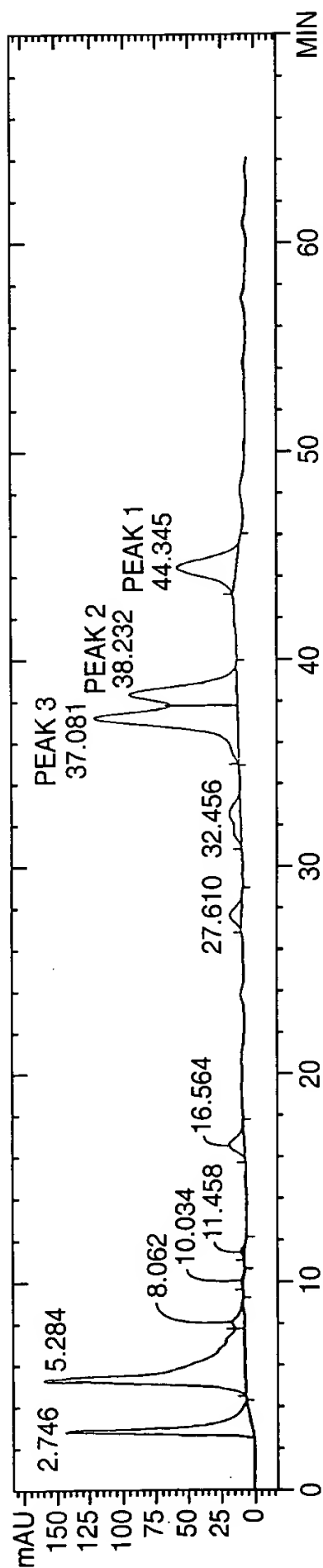
FIG.-2F

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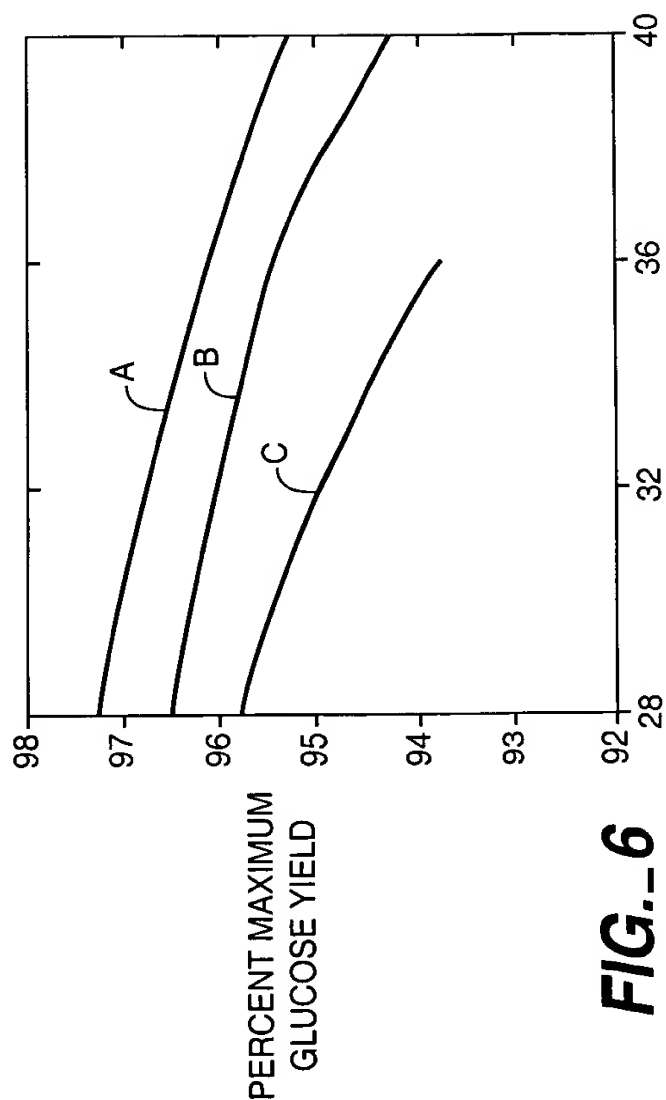
	D X N X X D W S R X X X	970	980	990	1000	Majority
824	D A V N E F D W S R K A Q					pullseqsig.seq.PRO
903	D W F N R V D Y S L Q D N N Y N V G M P R I S D D G S N Y E V I T R V K E M V A					klebpnseqsig.seq.pro
586	D S I N Q L D W D R R E T					subpull.seq.pro
	- - - - - X K X X X X Y Y X X L I X L R K X H P A F R L X X A X X I X X H L X	1010	1020	1030	1040	Majority
837	- - - - - Y P D V F N Y Y S G L I H L R L D H P A F R M T T A N E I N S H L Q					pullseqsig.seq.PRO
943	T P G E A E L K Q M T A F Y Q E L T E L R K S S P L F T L G D G S A V M K R V D					klebpnseqsig.seq.pro
599	- - - - - F K E D V H Y I R R L I S L R K A H P A F R L R S A A D I Q R H L E					subpull.seq.pro
	F L N X X E X - - - - - T V A Y X L X D X X X D X W - X X I I V X X N A	1050	1060	1070	1080	Majority
871	F L N S P E N - - - - - T V A Y E L T D H V N K D K W - G N I I V V Y N P					pullseqsig.seq.PRO
983	F R N T G S D Q Q A G L L V M T V D D G M K A G A S L D S R L D G L V V A I N A					klebpnseqsig.seq.pro
633	C L T L K E H - - - - - L I A Y R L Y D L D E V D E W - K D I I V I H H A					subpull.seq.pro
	X P X S X T X N L P X G X X X X X L X A X S G X X G E X T L X X - - - - - A X G	1090	1100	1110	1120	Majority
902	N K T V A T I N L P S G K - - W A I N A T S G K V G E S T L G Q - - - - - A E G					pullseqsig.seq.PRO
1023	A P E S R T L N E F A G E T L - Q L S A I Q Q T A G E N S L A N G V Q I A A D G					klebpnseqsig.seq.pro
664	S P D S V E W R L P N D I P Y R L L C D P S G F Q E D P T - - E - - - - - I K K					subpull.seq.pro
	T V X V P G - - I X X X I L X Q X X A X D X G - X K S X X - -	1130	1140	1150		Majority
935	S V Q V P G - - I S M M I L H Q E V S P D H G - K K - - - . K					pullseqsig.seq.PRO
1062	T V T L P A W S V A V L E L P Q G E A Q G A G L P V S S K					klebpnseqsig.seq.pro
697	T V A V N G - - I G T V I L Y - - L A S D L - - - K S F A					subpull.seq.pro

FIG.\_2G

**FIG.\_3A****FIG.\_3B**

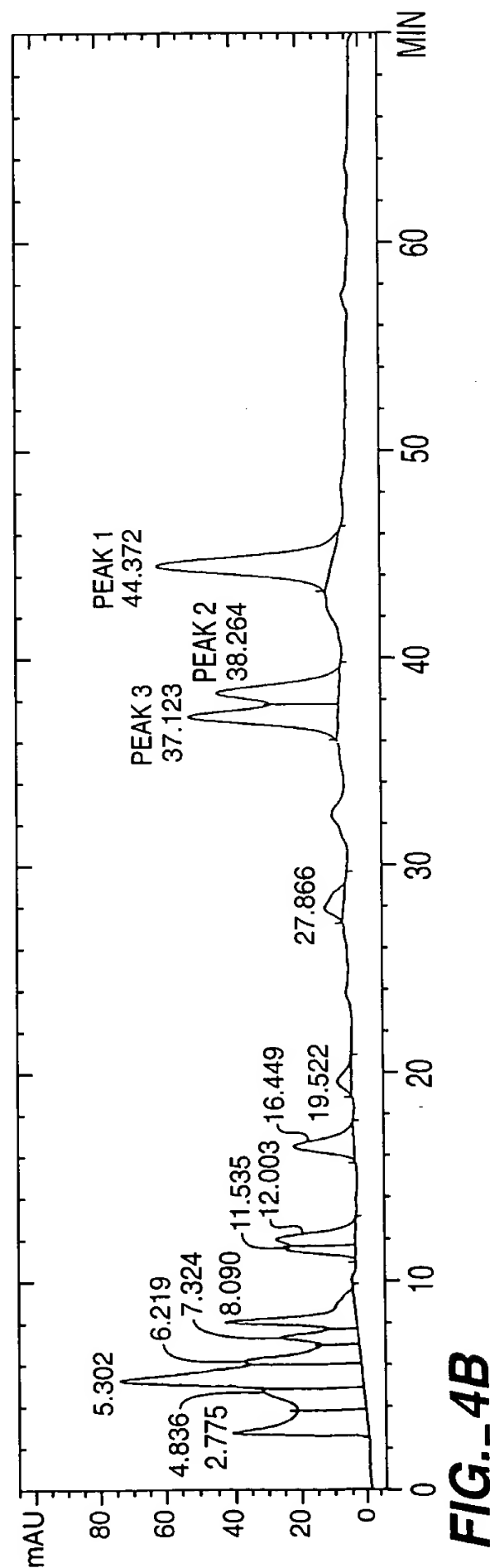
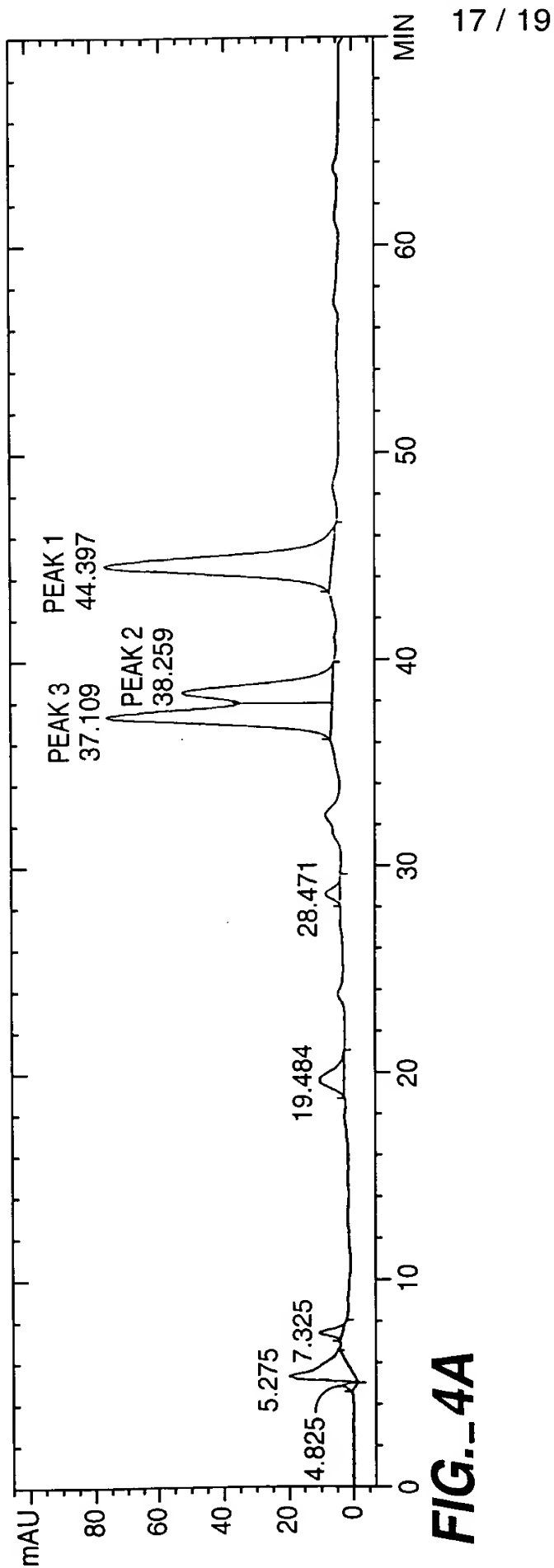


**FIG.-3C**



**FIG.-6**





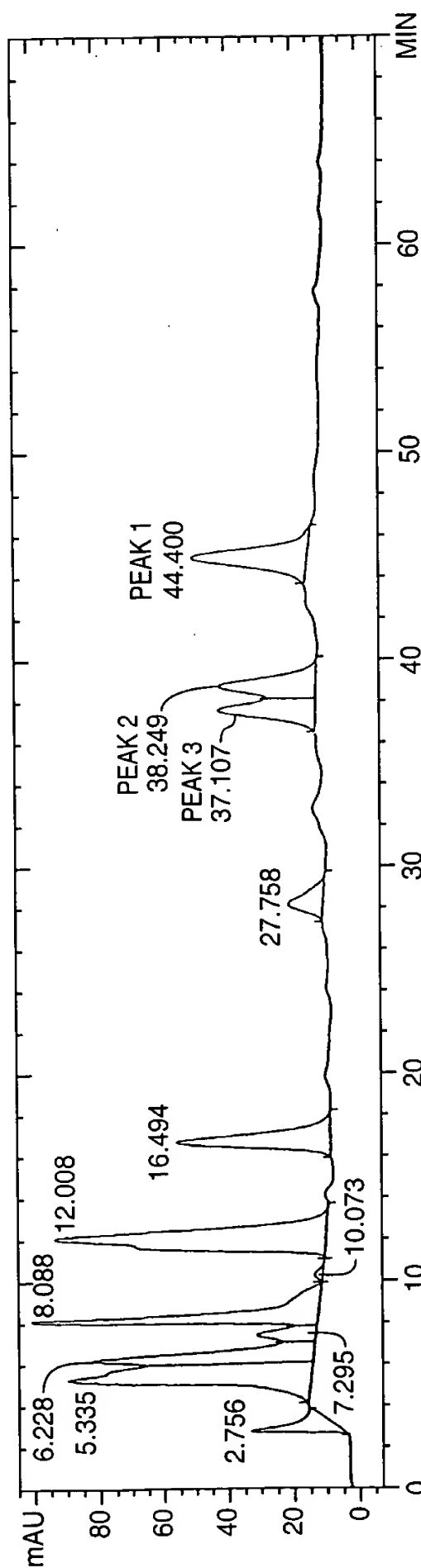


FIG. 4C

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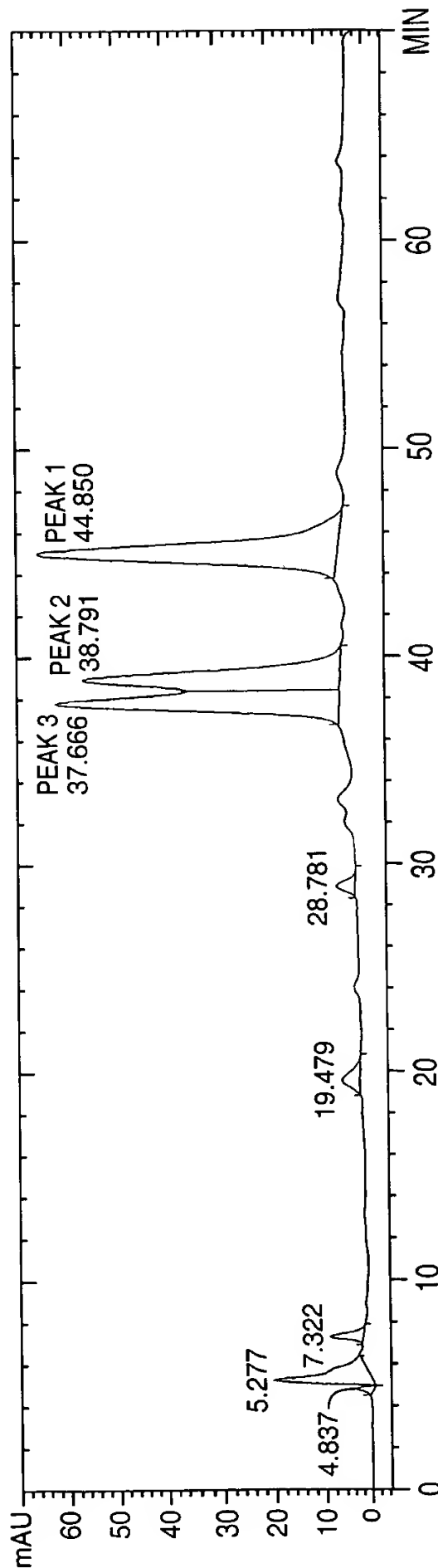


FIG. 4D

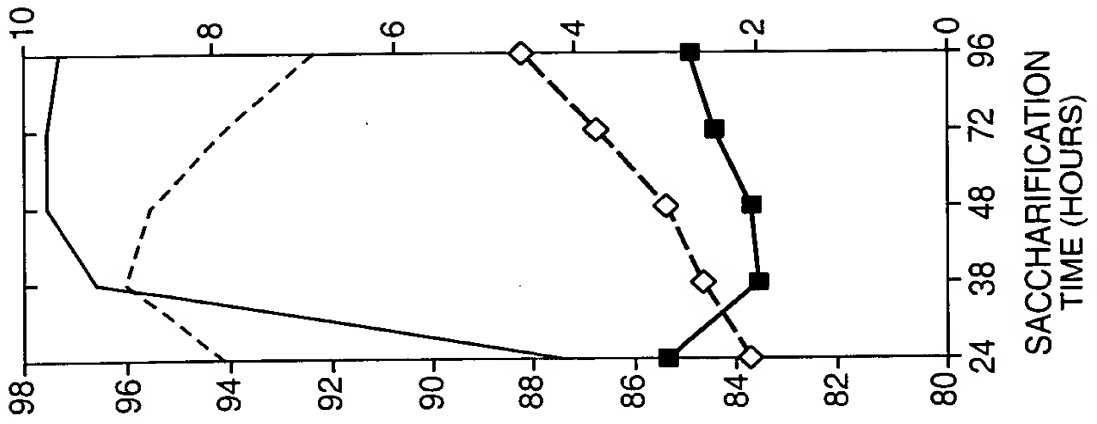


FIG. 5A

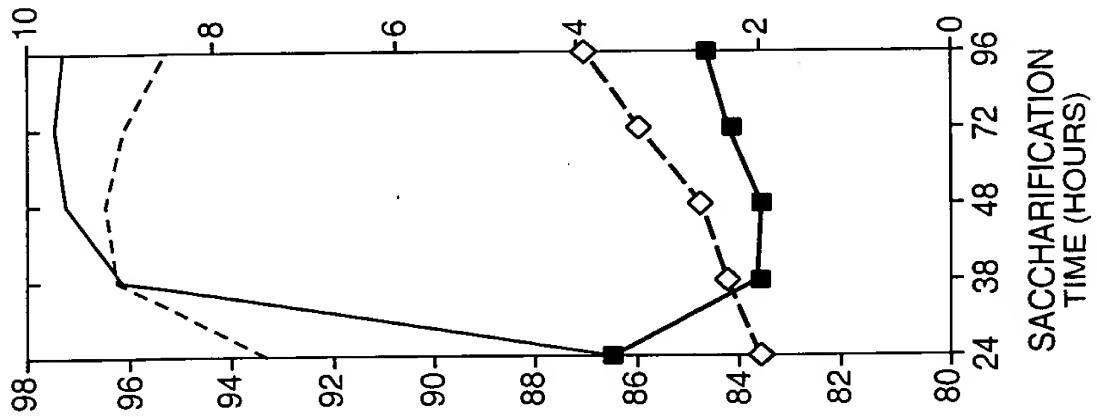


FIG. 5B

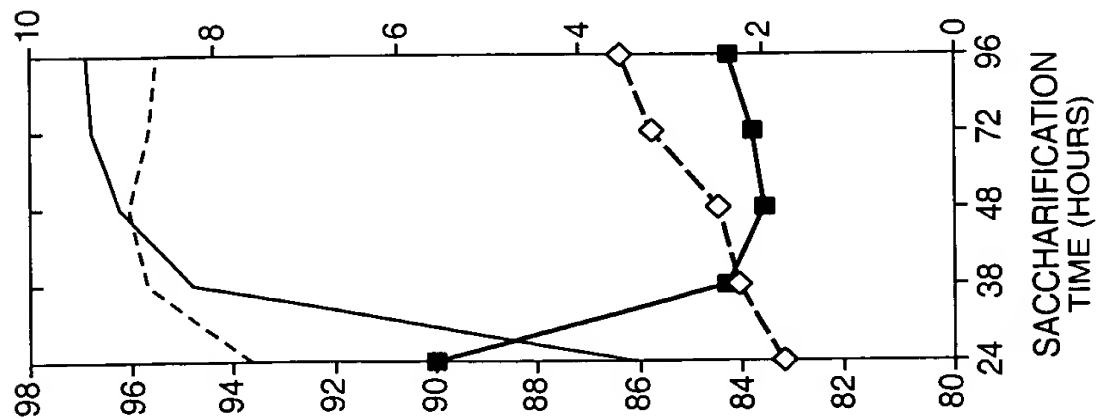


FIG. 5C